Hands On : Using MaBoSS with WebMaBoSS

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Computational Systems Biology for Complex Human Disease
from static to dynamic representations of disease mechanisms

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Using MaBoSS with WebMaBoSS

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› Creating a new simulation : Output nodes
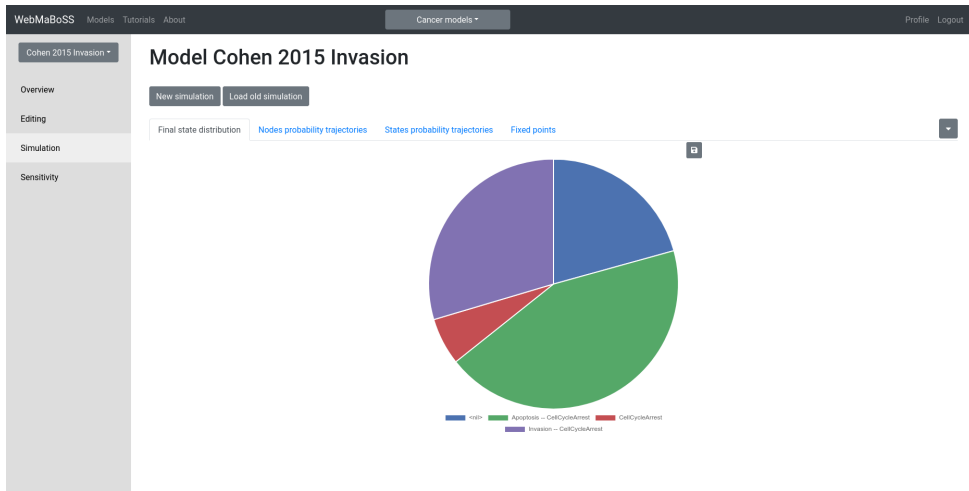
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› Creating a new simulation : Mutants

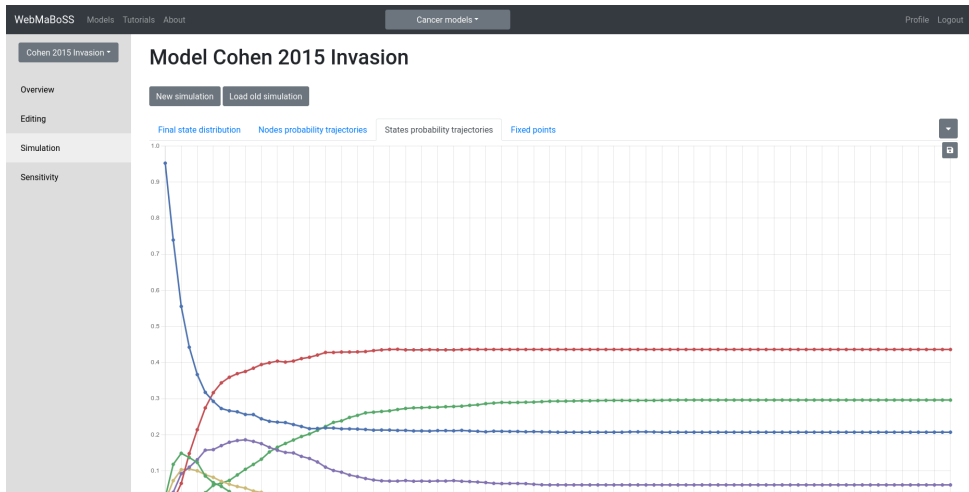# Using MaBoSS with WebMaBoSS

› Simulation results : Final states

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› Simulation results : Node trajectories

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› Simulation results : State trajectories

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› Simulation results : Fixed points

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› Model editing : (in)activation rules

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› Model editing : (in)activation rules

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› Model editing : Initial states

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› Model editing : Output nodes

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› Model editing : Parameters

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› Model editing : Settings

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› Sensitivity analysis : General settings

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› Sensitivity analysis : Mutant candidates

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› Sensitivity analysis : Output nodes

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› Sensitivity analysis : Results
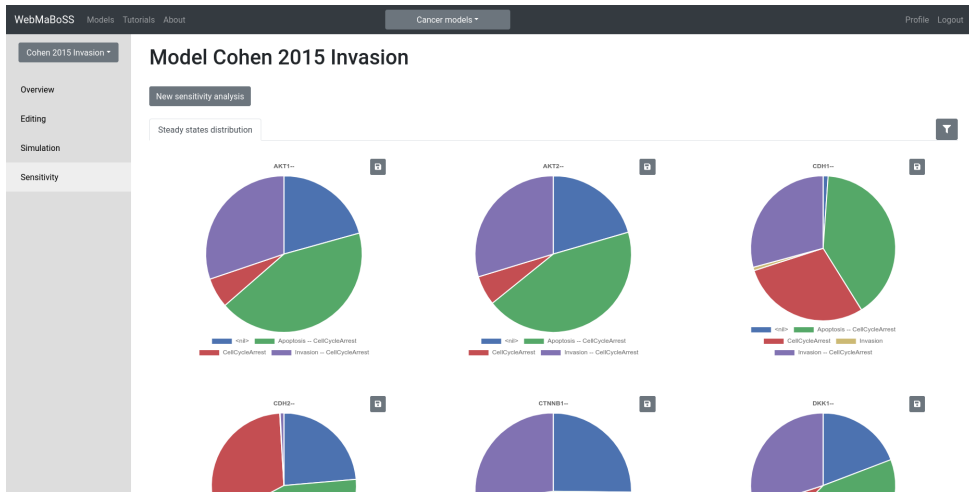
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› Sensitivity analysis : Filtering results

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› Sensitivity analysis : Filtered results

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› Hands on

    › Create a new project

    › Load Cohen's model (bnd and cfg available in manuals/Modules/MaBoss/ folder)

    › Perform default simulation

    › Perform simulation with ECMicroenv and DNADamage on

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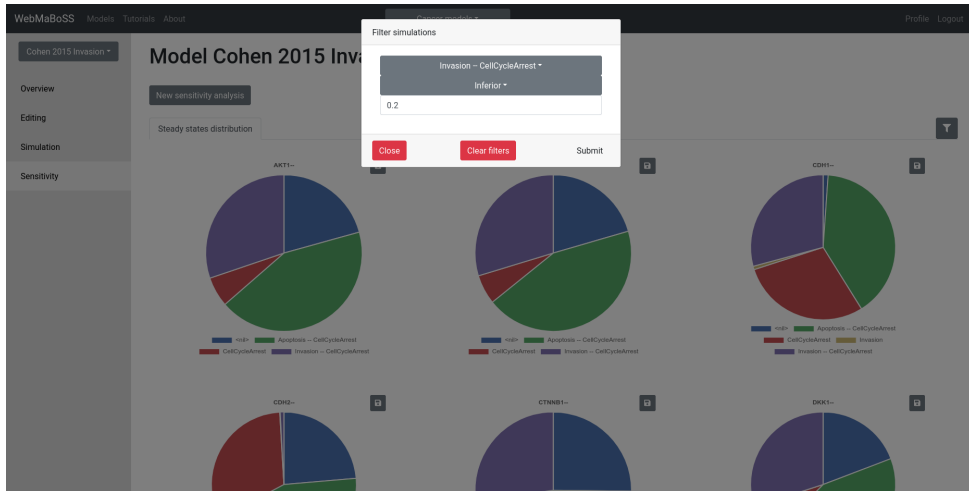
› Hands on

    › Perform simulation with NICD++, p53– mutant

    › Perform sensitivity analysis on single mutants, testing only inhibitions

    › Filter mutants where state Invasion – CellCycleArrest is less than 20%

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